

09987967.11601

CTCAACCACAGACTACACTTGCTGAACTGGCTCCTGGGGCCATGAGGCTGTCACTGCCAC
+-----+-----+-----+-----+-----+-----+
GAGTTGGTGTCTGATGTGAACGACTTGACCGAGGACCCCGTACTCCGACAGTGACGGTG
M R L S L P L

TGCTGCTGCTGCTGCTGGGAGCCTGGGCCATCCCAGGGGGCCTCGGGGACAGGGCGCCAC
+-----+-----+-----+-----+-----+-----+
ACGACGACGACGACGACCTCGGACCCGGTAGGGTCCCCCGGAGCCCTGTCCCGCGGTG
L L L L L G A W A I P G G L G D R A P L

TCACAGCCACAGCCCCACAACCTGGATGATGAGGAGATGTACTCAGCCACATGCCCGCTC
+-----+-----+-----+-----+-----+-----+
AGTGTCCGTGTCTGGGGTGTGACCTACTACTCCTCTACATGAGTCGGGTGTACGGGCGAG
T A T A P Q L D D E E M Y S A H M P A H

ACCTGCGCTGTGATGCCTGCAGAGCTGTGGCTTACCAGATGTGGCAAATCTGGCAAAGG
+-----+-----+-----+-----+-----+-----+
TGGACGCGACACTACGGACGTCTCGACACCGAATGGTCTACACCGTTTTAGACCGTTTCC
L R C D A C R A V A Y Q M W Q N L A K A

CAGAGACCAAACCTTCATACCTCAAACCTCTGGGGGGCGGGGGAAGTACGCGAGTTGGTCT
+-----+-----+-----+-----+-----+-----+
GTCTCTGGTTTGAAGTATGGAGTTTGAGACCCCCCGCCGCTTGACTCGCTCAACCAGA
E T K L H T S N S G G R R E L S E L V Y

ACACGGATGTCTTGGACCGGAAGTGTCTCCCGGAAGTGGCAGGACTACGGAGTTCGAGAAG
+-----+-----+-----+-----+-----+-----+
TGTGCCTACAGGACCTGGCCTTGACGAGGGCCTTGACCGTCTGATGCCTCAAGCTCTTC
T D V L D R N C S R N W Q D Y G V R E V

TGGACCAAGTGAAACGTCTCACAGGCCCAGGACTTAGCGAGGGGCCAGAGCCAAGCATCA
+-----+-----+-----+-----+-----+-----+
ACCTGGTTCACTTTGCAGAGTGTCCGGTCTGAATCGCTCCCCGGTCTCGGTTCTGAGT
D Q V K R L T G P G L S E G P E P S I S

CGGTGATGGTCACAGGGGGCCCTGGCCTACCAGGCTCTCCAGGACATGTTTGCACTACT
+-----+-----+-----+-----+-----+-----+
CGCACTACCAAGTGTCCCCCGGGGACCGGATGGTCCGAGAGGTCTGTACAAACGTGATGA
V M V T G G P W P T R L S R T C L H Y L

TGGGGGAGTTTGGAGAAGACCAGATCTATGAAGCCACCAACAAGGCCGAGGGGCTCTGG
+-----+-----+-----+-----+-----+-----+
ACCCCTCAAACCTCTTCTGGTCTAGATACTTCGGGTGGTTGTTCCGGCTCCCCGAGACC
G E F G E D Q I Y E A H Q Q G R G A L E

AGGCATTGCTATGTGGGGGACCCAGGGGGCCTGCTCAGAGAAGGTGTCAGCCACAAGAG
+-----+-----+-----+-----+-----+-----+
TCCGTAACGATACACCCCTGGGGTCCCCCGGACGAGTCTCTTCCACAGTCGGTGTCTC
A L L C G G P Q G A C S E K V S A T R E

FIG. 1A

09987967.111601

AAGAGCTCTAGTCCTGGACTCTACCCTCCTCTGAAAGAAGCTGGGGCTTGCTCTGACGGT
+-----+-----+-----+-----+-----+-----+
TTCTCGAGATCAGGACCTGAGATGGGAGGAGACTTTCTTCGACCCCGAACGAGACTGCCA
E L *

CTCCACTCCCGTCTGCAGGCAGCCAGGAGGGCAGGAAGCCCTTGCTCTGTGCTGCCATCC
+-----+-----+-----+-----+-----+-----+
GAGGTGAGGGCAGACGTCCGTCCGTCCCGTCCTTCGGGAACGAGACACGACGGTAGG

TGCCTCCCTCCTCCAGCCTCAGGGCACTCGGGCCTGGGTGGGAGTCAACGCCTTCCCTC
+-----+-----+-----+-----+-----+-----+
ACGGAGGGAGGAGGTCCGAGTCCCGTGAGCCCGGACCCACCCTCAGTTGCCGAAGGGGAG

TGGACTCAAATAAAACCCAGTGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
+-----+-----+-----+-----+-----+-----+
ACCTGAGTTTATTTTGGGTCACTGGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

FIG. 1B

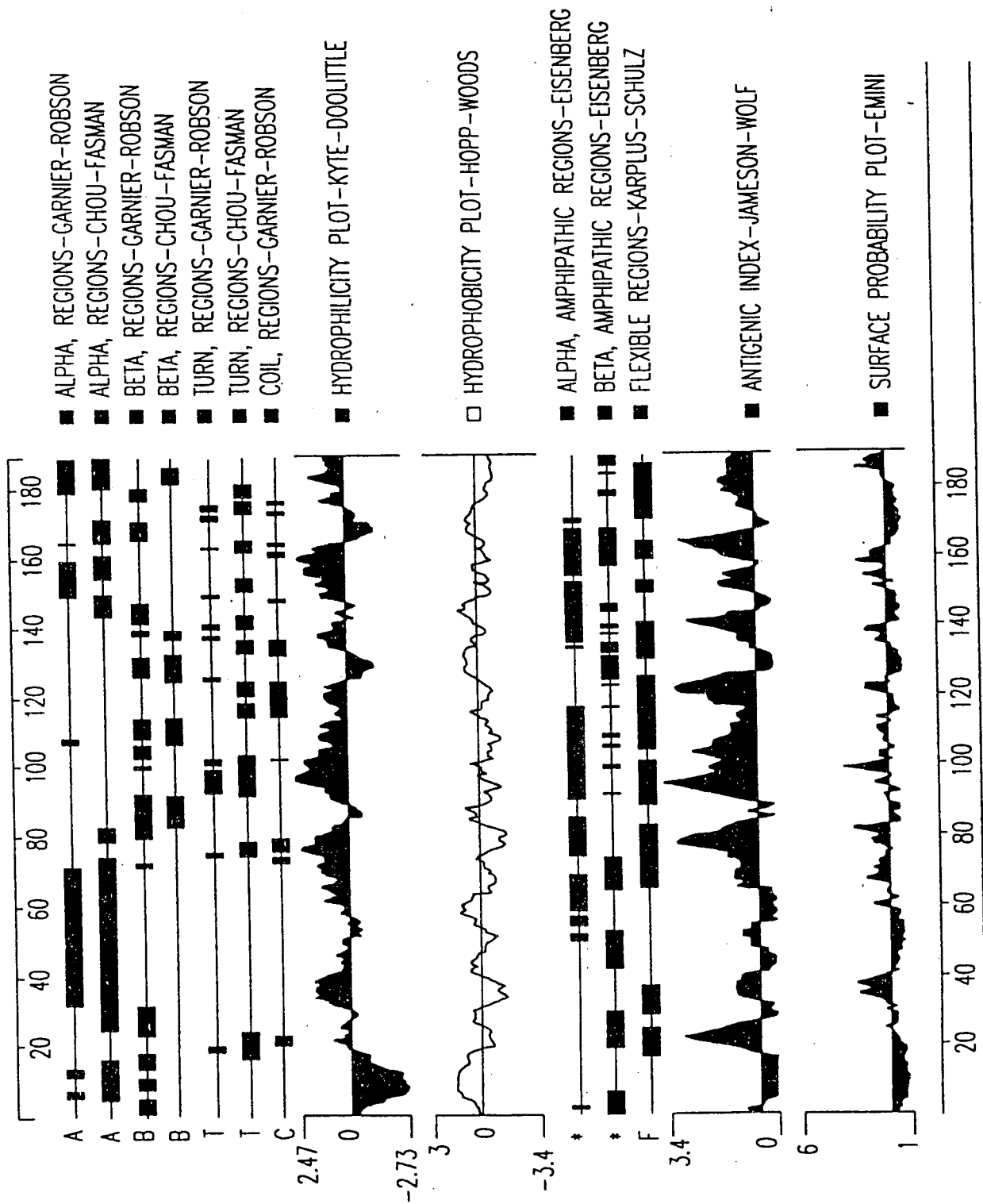


FIG.2